

CHAPTER 9

POPULATION SUBDIVISION

There is abundant geographical variation in both morphology and gene frequency in most species. The extent of geographic variation results from a balance of forces tending to produce local genetic differentiation and forces tending to produce genetic homogeneity.

Montgomery Slatkin (1987)

*The term "species" includes any subspecies of fish or wildlife or plants, and any **distinct population segment** of any species of vertebrate fish or wildlife which breeds when mature.*

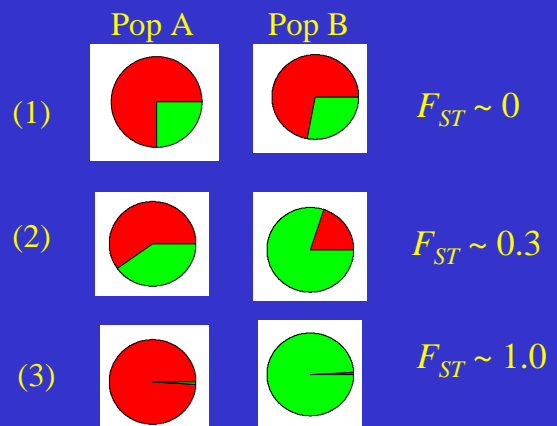
Endangered Species Act of the U.S.A.

Assumptions of Hardy-Weinberg model

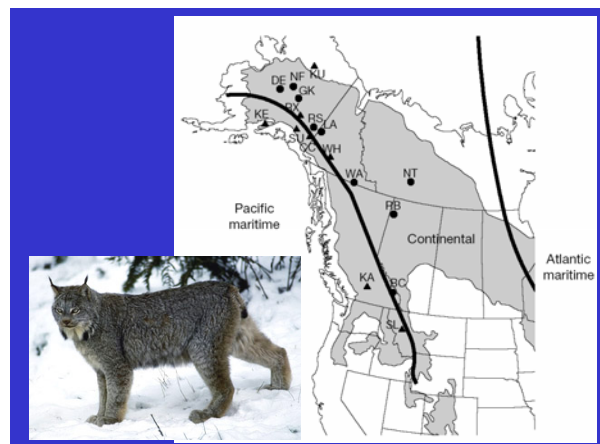
1. Random mating.
2. No mutation.
3. Large (infinite) population size.
4. No differential survival or reproduction (i.e., no natural selection).
5. No immigration

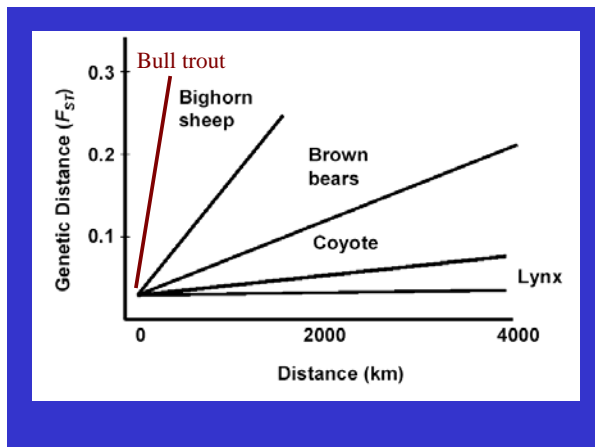
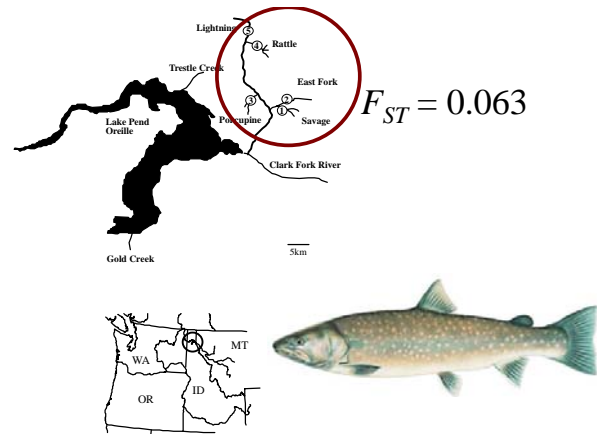
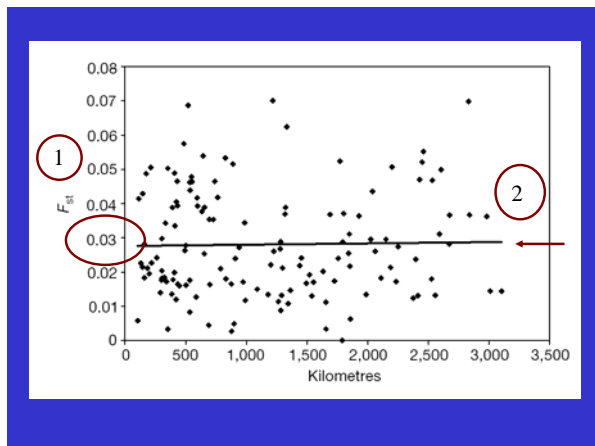
The total amount of genetic variation within a species (H_T) can be partitioned into genetic differences among individuals within populations (H_S) and genetic differences among different populations. The proportion of total genetic variation within a species that is due to differences among populations is represented by F_{ST} :

$$F_{ST} = 1 - \frac{H_S}{H_T}$$



Taxa	H_T	H_S	F_{ST}	No. species
Amphibians	0.136	0.094	0.315	33
Birds	0.059	0.054	0.076	16
Fish	0.067	0.054	0.135	79
Mammals	0.078	0.054	0.242	57
Reptiles	0.124	0.090	0.258	22
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Crustaceans	0.088	0.063	0.169	19
Insects	0.138	0.122	0.097	46
Mollusks	0.157	0.121	0.263	44



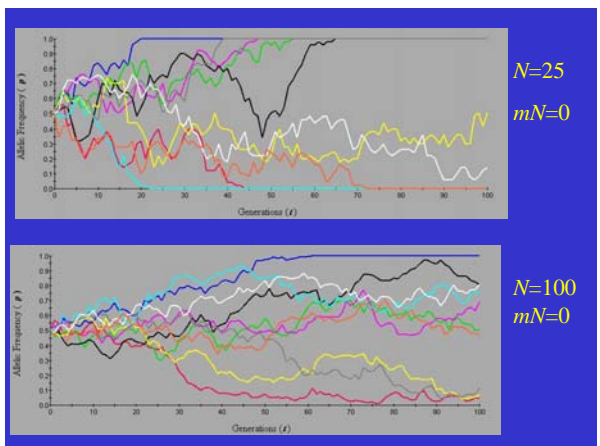
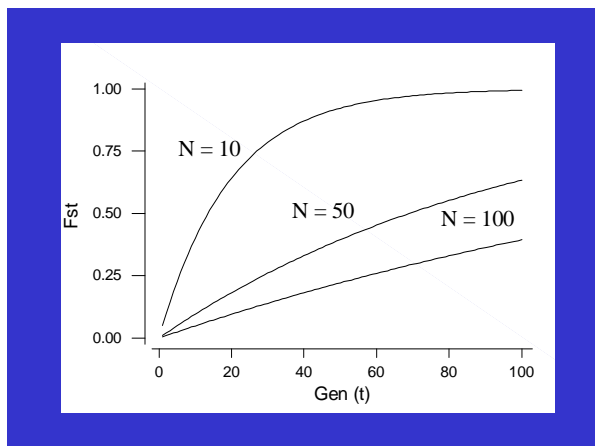


Complete Isolation

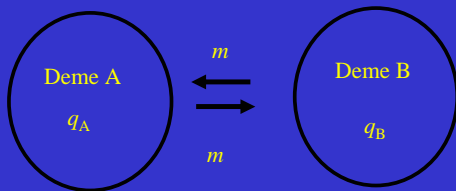
$$F_{ST} = 1 - \left(1 - \frac{1}{2N_e}\right)^t$$

(1) Eventual fixation

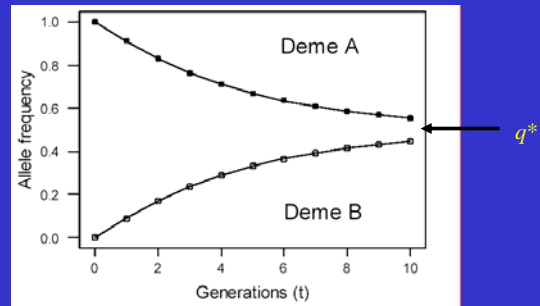
(2) Rate dependent upon N_e



Gene Flow



$$q'_A = (1 - m)q_A + mq_B$$

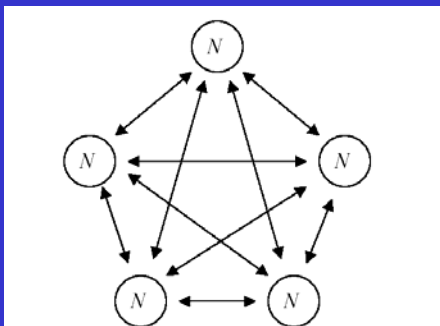


In general, there are two primary effects of gene flow:

- (1) Gene flow reduces genetic differences between populations.
- (2) Gene flow increases genetic variation within populations.

What happens if we combine gene flow and genetic drift?

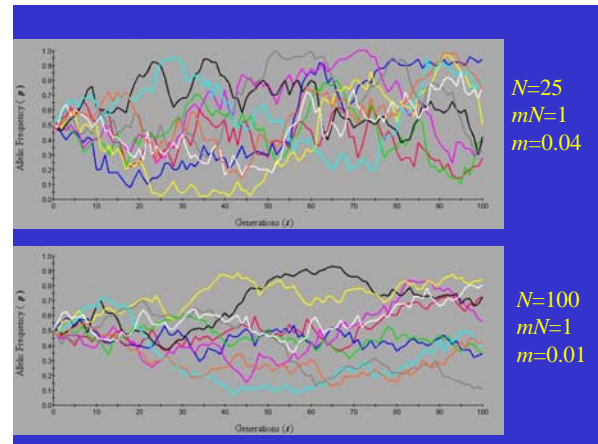
Island Model of Migration



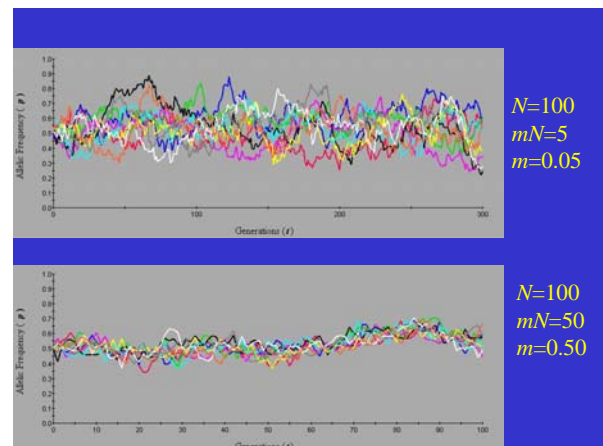
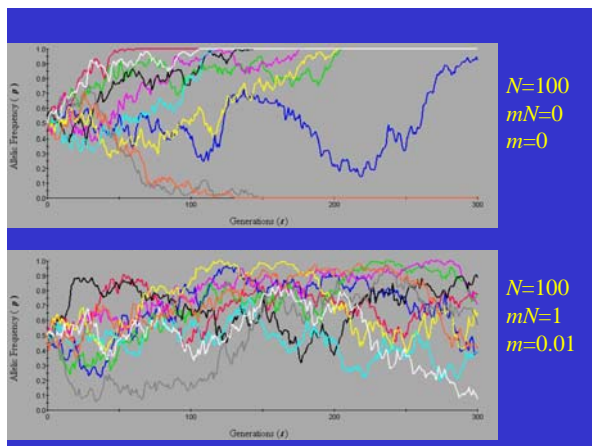
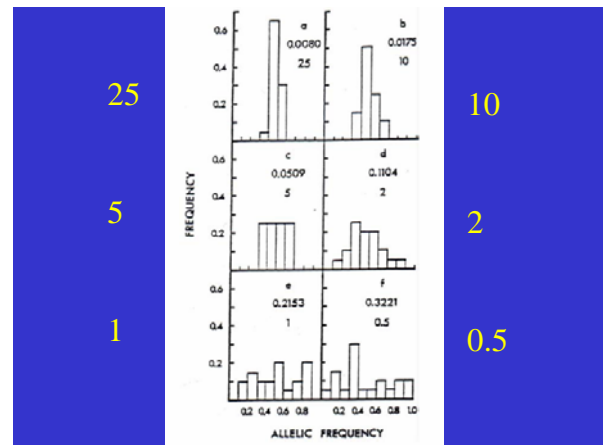
$$F_{ST}^* = \frac{(1 - m)^2}{[2N - (2N - 1)(1 - m)^2]} \quad F_{ST}^* \approx \frac{1}{(4mN + 1)}$$

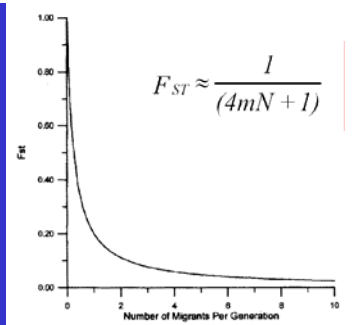
- (1) Divergence is dependent only on mN , not on the proportional contribution of migrants (m).
- (2) Even very little gene flow ($mN \sim 1$) can have a major effect on population structure.

(1) Divergence is dependent only on mN , not on the proportional contribution of migrants (m). mN is the number of migrant individuals per individual per generation.



(2) Even very little gene flow ($mN \sim 1$) can have a major effect on population structure.



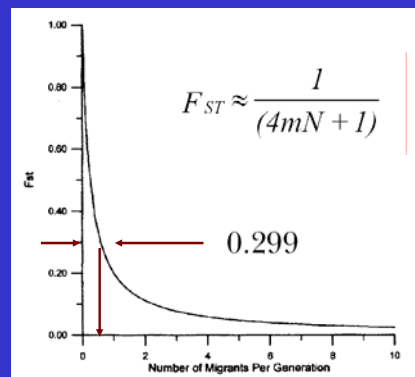
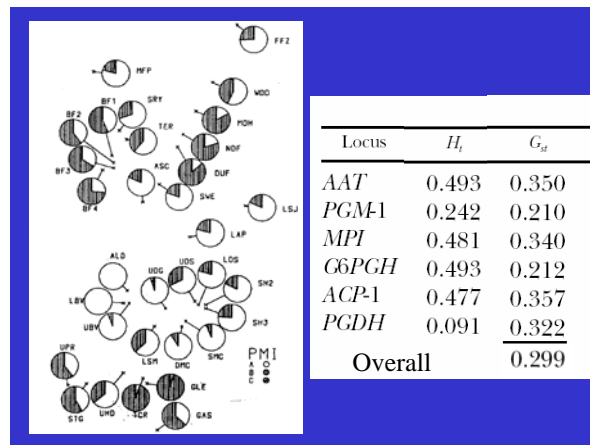
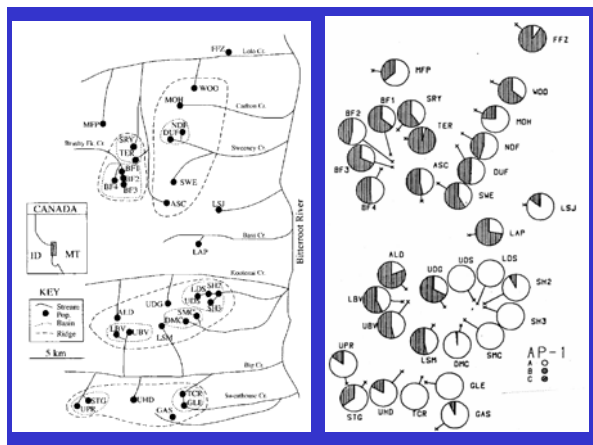


We can use this relationship to estimate gene flow among natural populations.

Long-toed salamander



Tallmon et al. Genetic differentiation among long-toed salamander (*Ambystoma macrodactylum*) populations. Copeia 27-35.

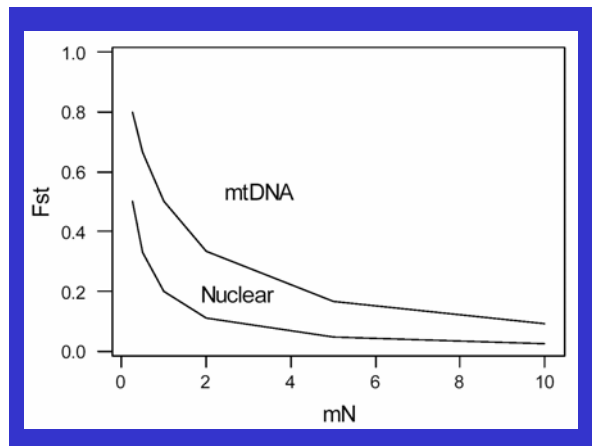


Mitochondrial DNA

The N_e of mtDNA is only one-quarter that of nuclear genes. Therefore,

$$F_{ST} \approx \frac{1}{(mN + 1)}$$

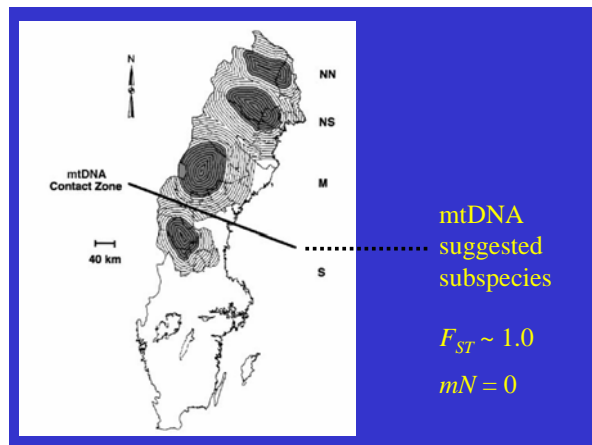
$$F_{ST} \approx \frac{1}{(2mN_F + 1)}$$



mtDNA versus nucDNA

Nuclear DNA microsatellite analysis of genetic diversity and gene flow in the Scandinavian brown bear (*Ursus arctos*)

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What happens if we combine natural selection along with genetic drift and gene flow?

Local adaptation

		A_1A_1	A_1A_2	A_2A_2
Demes 1-10		1	$1-t/2$	$1-t$
Demes 11-20		$1-t$	$1-t/2$	1

Local adaptation

	mN						N
	0.5	1	2	5	10	25	
Expected	0.3333	0.2000	0.1111	0.0476	0.0244	0.0099	
$t=0.00$	0.3070	0.2043	0.1245	0.0418	0.0198	-	25
	0.3350	0.1826	0.1077	0.0484	0.0264	0.0120	50
	0.3216	0.1884	0.1061	0.0437	0.0251	0.0095	100
$t=0.01$	0.3343	0.1703	0.1070	0.0556	0.0220	-	25
	0.2979	0.1192	0.1000	0.0381	0.0256	0.0099	50
	0.2997	0.1850	0.1146	0.0354	0.0229	0.0105	100
$t=0.05$	0.3560	0.1857	0.1204	0.0497	0.0217	-	25
	0.4618	0.2679	0.1489	0.0550	0.0265	0.0113	50
	0.5950	0.4230	0.1982	0.0632	0.0207	0.0118	100
$t=0.10$	0.4700	0.2446	0.1632	0.0473	0.0289	-	25
	0.6242	0.3653	0.2611	0.0771	0.0356	0.0128	50
	0.8054	0.6575	0.4432	0.1589	0.0632	0.0193	100

Natural selection + drift + gene flow

1. Divergence no longer a function of only mN .
2. Large differences among loci can be produced by even fairly weak natural selection.
3. The larger the local N_e , the more effective natural selection is.

Population “Genomics”

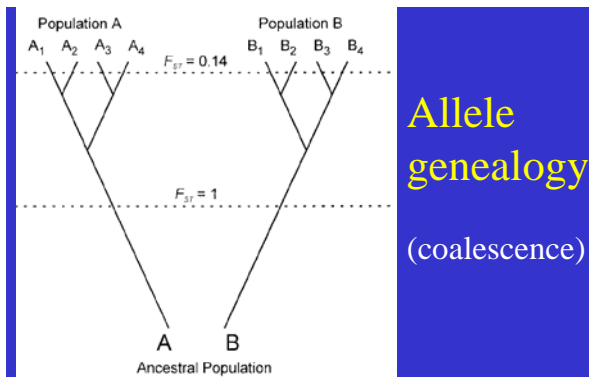
Estimate divergence (F_{ST}) at many loci. Outlier loci are “candidates” for natural selection.

Beyond F_{ST} :

Other measures of population divergence

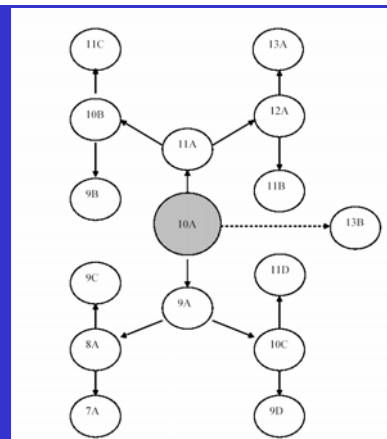
F_{ST} is not a good measure if within population variation (H_S) is high, as with microsatellites.

$$F_{ST} = 1 - \frac{H_S}{H_T}$$



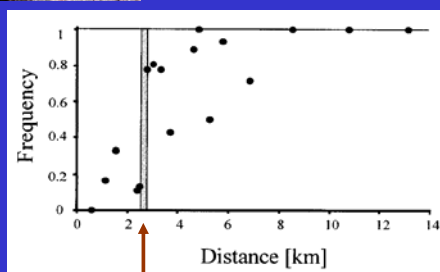
R_{ST} is an analogue of F_{ST} that takes the relative size of alleles (i.e., allelic state) into consideration.

Microsatellite mutation network



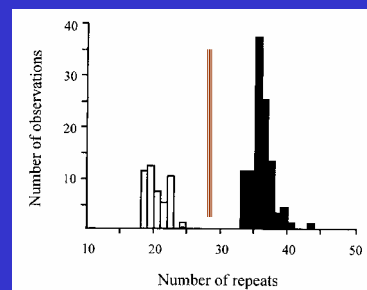
Common shrew in western France

mtDNA



Hybrid zone

Y-linked microsatellite locus



$H_S = 0.71$

$F_{ST} = 0.19$; $R_{ST} = 0.98$